RAW SEQUENCE LISTING
PATENT APPLICATION **US/09/087,136A**

DATE: 05/08/2000
TIME: 18:16:39

Input Set: **I087136A.RAW**

> This Raw Listing contains the General Information
> Section and up to first 5 pages.

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 2    <120> TITLE OF INVENTION: A TUMOR SUPPRESSOR PATHWAY IN C. ELEGANS
 3    <130> FILE REFERENCE: 01997/202002
 4    <140> CURRENT APPLICATION NUMBER: US/09/087,136A
 5    <141> CURRENT FILING DATE: 1998-05-28
 6    <150> EARLIER APPLICATION NUMBER: 60/047,996
 7    <151> EARLIER FILING DATE: 1997-05-28
 8    <160> NUMBER OF SEQ ID NOS: 18
 9    <170> SOFTWARE: FastSEQ for Windows Version 4.0
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11    <211> LENGTH: 275
12    <212> TYPE: PRT
13    <213> ORGANISM: Caenorhabditis elegans
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18                      20                  25                  30
19         Pro Leu Glu Ser Pro Ser Arg Lys Leu Thr Ser Leu Leu Ser Tyr Asp
20                      35                  40                  45
21         Pro Thr Val Pro Glu Ser Pro Asp Met Lys Phe Ala Arg Lys Arg Leu
22                      50                  55                  60
23         Gly Asn Leu Leu Thr Thr Ile Lys His His Pro Ser Glu Ile Ile Gly
24         65                  70                  75                  80
25         Val Leu Pro Glu Asp Tyr Thr Arg Ala Asp Glu Glu Pro Gly Arg Gln
26                      85                  90                  95
27         Gly Arg Pro Pro Gly Arg Pro Arg Lys Met Pro Arg His Glu Ser Ser
28                      100                 105                 110
29         Thr Ser Leu Met Glu Ser Pro Arg Lys Thr Met Thr Arg Asp Ser Lys
30                      115                 120                 125
31         Ile Met Phe Glu Leu Arg Gly Lys Pro Phe Glu Met Ile Ala Gly Arg
32                      130                 135                 140
33         Phe Glu Glu Glu Tyr Ser Leu Gly Arg Ala Trp Val Lys Gly His Met
34         145                 150                 155                 160
35         Asn Asn Glu Tyr Glu Pro Ile Lys Ala Gln Arg Thr Asp Tyr Ala Pro
36                      165                 170                 175
37         Asn Leu Ala Val Asp Tyr Leu Ala Cys Arg Glu Ile His Arg Met Pro
38                      180                 185                 190
39         Arg Pro Asp Lys Ser Ile Pro Glu Leu Pro Ile Val Pro Ser Arg Ile
40                      195                 200                 205
41         Asp Glu Phe Asp Ala Thr Val Asp Pro Arg Tyr Glu Thr Asp Leu Lys
42                      210                 215                 220
43         Asn Glu Tyr Ile Arg His Trp Lys Gln Val Lys Lys Gly Trp Cys Ala
44         225                 230                 235                 240
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45	His Gln Arg Arg Arg Thr Ala Pro His Ala Arg Ser Ile Ala Leu Ile
46	245 250 255
47	Asn Lys Ile Tyr Gln Pro Gly Glu Ser Lys Thr Val Glu Gln Ala Leu
48	260 265 270
49	Gly Leu Ile
50	275
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52	<211> LENGTH: 954
53	<212> TYPE: DNA
54	<213> ORGANISM: Caenorhabditis elegans
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58	ctcacatccc tgttatccta tgatccgaca gttccggagt caccggatat gaaattcgcc	180
59	agaaaacgtc tgggaaatct gctgacaacc ataaaacatc acccatcgga aataattgga	240
60	gtactcccag aagattatac tcgtgctgat gaagagcccg ggcgccaagg acgtccacca	300
61	ggtcgccctc gtaagatgcc gcgtcacgaa tcttcaactt cacttatgga atcaccacgc	360
62	aagactatga ctcgtgattc taaaattatg tttgaattgc gtggaaaacc attcgaaatg	420
63	atagctggac gttttgaaga agaatattca cttggtagag catgggttaa aggacacatg	480
64	aataatgaat atgaaccaat aaaagctcaa aggacagact atgcaccgaa tctggctgtt	540
65	gattatcttg catgtcgcga gattcatcga atgccacgtc cagataaatc aattcctgag	600
66	ctgccaattg ttccatctag aatcgatgaa ttcgacgcta cagtcgatcc aagatatgaa	660
67	acagatttga aaaatgaata cattcgtcat tggaaacaag tcaaaaaagg ttggtgtgct	720
68	catcaacgtc gtcggactgc tccccatgca agaagcatag cattaatcaa caaaatctac	780
69	cagcctggag agtcgaaaac tgtcgagcaa gcacttggtc ttatttaaat attctaacat	840
70	gtaatttcaa tttatctctt actttctgat cttgctatca catgtctctt atttcaaaaa	900
71	tctcacttta aaattcatat aaataatggg tttattcaaa tacatcatct tgac	954

72	<210> SEQ ID NO 3
73	<211> LENGTH: 961
74	<212> TYPE: PRT
75	<213> ORGANISM: Caenorhabditis elegans
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79	Phe His Glu Gln Ser Pro Phe Asp Ala Val Leu Ala Gly Thr Glu Thr
80	20 25 30
81	Thr Asp Thr Ile Cys Glu Glu Pro Pro Ala Lys Arg Ile Asp Leu Asp
82	35 40 45
83	Ile Lys Gln Glu Phe Asn Gly Gly Val Gln Ser Gly Gly Leu Ile Lys
84	50 55 60
85	Asn Glu Ser Glu Leu Thr Gln Met Thr Ile Lys Gln Glu Thr Glu Gly
86	65 70 75 80
87	Asn Ile Asn Glu Ala Arg Arg Glu Glu Glu Asp Glu Glu Gln Asp Glu
88	85 90 95
89	Asp Ser Arg Thr Ser Met Pro Pro Ala Leu Gly Glu Asp Asp Asp Tyr
90	100 105 110
91	Glu Glu Asp Asp Ala Asp Ser Phe Ile Asp Lys Thr Asn Thr Pro Pro
92	115 120 125
93	Pro Ser Gln Ser Phe Leu Glu Gly Cys Arg Ala Ala Asn Leu Pro Asn
94	130 135 140

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 97     Val Ser Leu Glu Gly Ser Glu Ser Ala Trp Gln Leu Ser Ala Ile Tyr
 98                     165             170             175
 99     Tyr Tyr Leu Leu Ser Lys Gly Ile Lys Arg Arg Gly Lys Thr Ile Arg
100                     180             185             190
101     Ile Leu Ile Gln Pro Phe Pro Val Ser Ile Leu Thr Ile Ala Asn Ser
102                     195             200             205
103     Phe Asp Ile Ser Val Ala Glu Met Leu Asp Lys Thr Ala Arg Phe Val
104         210             215             220
105     Glu Ile Ile His Ser Arg Lys Ile Arg Arg Tyr Gln Glu Tyr Ile Arg
106     225             230             235             240
107     Arg Ile Gln Glu Gly Leu Ala Val Ser Cys Val Ile Phe Lys Lys Phe
108                     245             250             255
109     Cys Arg Ile Phe Cys Lys Ile Phe Glu Glu Ile Lys Val Gly Ser Glu
110                     260             265             270
111     Asn Cys Pro Ser Ser His Glu Leu Phe Thr Val Leu Trp Thr Ser Phe
112                     275             280             285
113     Leu Val Met Lys Ser Arg Met Thr Val Asp Asp Leu Ile Ser Asn Tyr
114         290             295             300
115     Gln Leu Leu Phe Ser Ile Leu Asp Gln Val Tyr Thr Glu Met Cys Ser
116     305             310             315             320
117     Met Lys Glu Gly Ile Val His His Leu Asn Gln Lys Phe Val Glu Asp
118                     325             330             335
119     Leu Leu Glu Asn Asp Cys Thr Ile Ile Arg Ala Leu Cys Thr Gln Phe
120                     340             345             350
121     Gly Gly Ser Val Leu Asp Ala Arg His Phe Ser Asp His Thr Phe Lys
122                     355             360             365
123     Lys Met Glu Lys Thr Gly Ile Pro Ser Thr Trp Asn Phe Gln Glu Phe
124         370             375             380
125     Arg Asp Leu Ile Met Asn Val Pro Lys Thr Ala Tyr Glu Asn Tyr Leu
126     385             390             395             400
127     Leu Gln Arg Gly Ser Ile Asp Glu Arg Ile Phe Ile Pro Ser Val Glu
128                     405             410             415
129     Asp Phe Ser Lys Ile Phe Gln Ser Pro Asp Thr Tyr Ser Val Ala Asp
130                     420             425             430
131     Ile Leu Lys Val Ser Tyr Ser Gly Arg Arg Phe Arg Asp Ala Glu Phe
132                     435             440             445
133     Leu Thr Lys Ile Ser Asn Asn His Cys Leu Glu Lys Leu Ala Leu Gly
134         450             455             460
135     Gly Lys Val Ala Ser Glu Lys Leu Val Thr Gln Ser Lys Glu Gln Pro
136     465             470             475             480
137     Arg Val Pro Cys Val Glu Tyr Asn Leu Glu Leu Gly Asn Tyr Pro Asp
138                     485             490             495
139     Asp Leu Glu Ser Asn Asn Gln Ser Leu Tyr Asn Arg Leu Thr Lys Ile
140                     500             505             510
141     Ile Gly Ser Trp Lys Leu Glu Asn Ser Lys Leu Glu Glu Val Cys Gly
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143     Thr Met Ser Asp Ser Pro Met Ala Thr Ile Leu Leu Lys Ser Asp Glu
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145          Met Thr Asn Lys Phe Glu Arg Thr Leu Ser Ala Glu Leu Gly Glu Thr
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147          Ile Asn Glu Asn Ile Pro Lys Tyr His Tyr Asn Val Arg Lys Glu Leu
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149          Glu Leu Val Phe Leu Ile Phe Met Glu Lys Ile Ile Val Ala Glu Leu
150                      580             585             590
151          Lys Lys Lys Val Arg Glu Glu Asp Leu Leu Asn Val Ile Arg Arg Glu
152                      595             600             605
153          Glu Phe Leu Asp Ser Val Phe Cys Phe Cys Val Glu Leu Ile Leu Val
154              610             615             620
155          Ser Asn Gly Tyr Asp Arg Pro Phe Pro Trp Ser Ala Glu Leu Cys Gly
156          625             630             635             640
157          Val His Pro Phe Met Phe His Lys Val Ile Asp Leu Met Ile Thr His
158                      645             650             655
159          Glu Lys Gln Leu Ser Arg Gln Met Val Gln His Phe Ser Arg Ile Glu
160                      660             665             670
161          Glu Thr Val Ile Glu Tyr Phe Ser Trp Lys Ser Asp Ser Pro Leu Trp
162                      675             680             685
163          Pro Met Val Val Arg Cys Pro Phe Ala His Phe Gln Glu Phe Gly Glu
164              690             695             700
165          Asp Trp Ala Asp Lys Leu Asn Ser Tyr Ser Pro Ile Lys Phe Thr Pro
166          705             710             715             720
167          Ile Lys Lys Pro Asp Asp Leu Arg Asp Glu Leu Gly Arg Pro Ile Val
168                      725             730             735
169          Pro Gln Asn Gln Thr Ser Arg Thr Leu Arg Ile Phe Leu Lys Arg Thr
170                      740             745             750
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173          Met Gly Ala Arg Ala Lys Ser Gln Cys Trp Ser Leu Phe Asp Tyr Leu
174              770             775             780
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177          Leu Leu Cys Cys Val Phe Val Ile Met Lys Ile Asn Glu Ser Ser Met
178                      805             810             815
179          Leu Phe Thr Glu Ile Met Ala Gln Tyr Arg Arg Gln Ser Ala Asn Ser
180                      820             825             830
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182                      835             840             845
183          Glu Asn Pro Gln Ala Val Asn Thr Lys Glu Thr Ile Leu Glu Arg Leu
184              850             855             860
185          Glu Gly Pro Gln Lys Glu Lys Thr Thr Val Asp Ile Ile Lys Tyr Tyr
186          865             870             875             880
187          Asn Ile Glu Phe Arg Asp Arg Ile Lys Tyr Ile Ile Gly Gln Ile Asp
188                      885             890             895
189          Ser Ala Ser Asp Glu Asp Leu Met Glu Met Pro Val Ala Thr Glu Ser
190                      900             905             910
191          Gly Leu Met Pro Val Arg Val Tyr Leu Thr His Lys Leu Ser Ile Gln
192                      915             920             925
193          Thr Leu Pro Lys Thr Lys His Gly Glu Ser Lys Gln Glu Arg Ala Ile
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205        ccagcaaaac gaatcgactt agatataaag caagaattca atggtggagt gcaaagtgga   180
206        gggctgatta aaaatgaatc cgaattgact caaatgacaa tcaaacaaga aacagaagga   240
207        aacataaatg aagctagacg agaagaagaa gacgaagaac aagatgaaga ttccagaaca   300
208        tcaatgccac ctgcattggg agaagatgat gattatgagg aggatgatgc tgatagtttt   360
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